FIG. 1 (1 of 4)

20	17 100	34 150	50	67 250	84 300	100	117		·
ATGGCGCCGTCCTCCCTGGAACAGAAGCTGTCCCGCCTGGAAGCAAAGCT	MetAlaAlaSerSerLeuGluGlnLvsLeuSerAraLeuGluAlaLvsLe GAAGCAGGAGAACCGGGAGGCCCGGCGAGGATCGACCTCAACCTGGATA	ULYSGINGIUASNArgGluAlaArgArgArgIleAspLeuAsnLeuAspI ULYSGINGIUASNArgGluAlaArgArgArgIleAspLeuAsnLeuAspI TCAGCCCCCAGCGCCCAGGCCCATTATTGTGATCACTCTAAGCCCTGCT	lelelelelelelelelelelelelelelelelelele	ProAlaProSerGlnArgAlaAlaLeuGlnLeuProLeuAlaAsnAspGl GGGCAGCCGCTCGCCATCCTCAGAGAGCTCCCCGCAGCACCCCACGCCCC	yGlySerArgSerProSerSerGluSerSerProGlnHisProThrProP CCGCCCGGCCCCGCCATGCTGGGGCTCCCGTCAACCCTGTTCACACCC	roalaargProargHisMetLeuGlyLeuProSerThrLeuPheThrPro cgcagcaTggagagcaTTgagaTTgaccagaagcTgcaggagaTcaTgaa	ArgSerMetGluSerIleGluIleAspGlnLysLeuGlnGluIleMetLy		
⊢	1 2 - 1	1 7 1	175	1 2	1 7 1 -	1 7 1	7	e	
NO:									
	NO:	N N O N	NO NO	NO:	NO NO	NO NO	NO:		
Π	H H	H			H H	OI OI	ij		
SEQ	SEQ SEQ	SEQ SEQ	SEQ SEQ	SEQ SEQ	SEQ SEQ	SEQ SEQ	SEQ		

FIG. 1 (2 of 4)

 	TG 450	 al 150	AT 500	 Me 167	GG 550	 uA 184	GG 600	11 1y 200	AC 650	Th 217	CA 700	 gI 234
sGlnThrGlyTyrProThrIleGlyGlyGlnArgTyrGlnAlaGluIleA	ACGACCTGGAGAACTTGGGCGAGATGGGCAGCGGCACCTGCGGCCAGGTG		TGGAAGATGCGCTTCCGGAAGACCGGCCACGTCATTGCCGTTAAGCA		GCGGCGCTCCGGGAACAAGGAGGAGAACAAGCGCATCCTCATGGACCT		ATGTGGTGCTGAAGAGCCACGACTGCCCCTACATCGTGCAGTGCTTTC		ACGTTCATCACCAACACGGACGTCTTCATCGCCATGGAGCTCATGGGC		CTGCGCTGAGAAGCTCAAGAAGCGGATGCAGGGCCCCATCCCGAGCC	
2	1	2 -	1	2	- - -	2	<u>⊢</u>	2	- - -	2 -	⊢	2
NO:	NO:	NO:	NO:	NO:	NO:	NO:	NO:	NO:	NO:	NO:	NO:	NO:
N QI	N QI	N QI	Z QI	ID N	N OI	N QI	N O I	N QI	N QI	N QI	I O I	N QI
SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ	SEQ

STACTACCTGAAA 	TGGTGGACTCCAAAGCCAAGACGCGGAGCGCCGGCTGTGCCGCCTACATG	GCACCCGAGCGCATTGACCCCCAGACCCCACCAAGCCGGACTATGACAT	CCGGCCCGACGTATGGAGCCTGGGCATCTCGTTGGTGGAGCTGGCAACAG CCGGGCCGACGTATGGAGCCTGGGCATCTCGTTGGTGGAGCTGGCAACAG CCGGGCCGACGTATGGAGCCTGGGCATCTCGTTGGTGGAGCTGGCAACAG CAGGACGACGTATGGAGCCTGGGCATCTCGTTGGTGGAGCTGGCAACAG CAGGACAAAAAAAAAA	GACAGTTTCCCTACAAGAACTGCAAGACGGACTTTGAGGTCCTCACCAAA
in it is at it	GAGCGCCGGCTGT	CCCACCAAGCC	TCGTTGGTGG;	GACTTTGAGG
TGAAGGCGCTC AllysalaLet GTCAAGCCCTC CTCAAGCCCTC SVallysProse GGACTTCGGC7 rsAspPheGly]	G — G	· · · · · ·	بار <u>ت</u> — م	2 <u>—</u> 4
CAGTGGCGATTC hrValAlaile\ ATCCACCGCGAC	CCAAGACGCG	GACCCCCAGAC	aspriorioasp gagccTGGGCAT 	AGAACTGCAAGA ysAsnCysLysT
TTCTGGGCAAGATGACAGTGGCGATTGTGAAGGCGCTGTACTACCTGAAA	GTGGACTCCAAAG	ACCCGAGCGCATT	GGGCCGACGTATG	CAGTTTCCCTACA GlnPheProTyrL
	<u> </u>	j <u>G</u> (- G - G - Z
7 7 7 7 7 7	4 ~	1 4 6	2 1	Н 0
NO: NO: NO: NO:	NO:		NO:	NO:
SEQ SEQ SEQ SEQ SEQ	SEQ	SEQ SEQ	SEQ SEQ	SEQ SEQ

FIG. 1 (4 of 4)

 eArgStop 435	rGluSerProArgThrSerGlyValLeuSerGlnProHisLeuProPhePheArgStop 435	2		ID NO:		SEQ
CAGGTAG 1308	TGAGTCAC	1		NO:	ID	SEQ
417		2		NO:	ID	SEQ
1250		·		NO:	ID	SEQ
400		2		NO:	ID	SEQ
1200	ATAATAAGCTACTTGAACACAGCTTCATCAAGCGCTACGAG	Η.		NO:	G	SEQ
384		7		NO:		SEQ
1150	GGACTTCC	⊢		NO:	ID	SEQ
367	SEQ ID NO: 2 - ValLeuGlnGluGluProProLeuLeuProGlyHisMetGlyPheSerGl 367	7		NO	ID	SEQ
1100	GTCCTACAGGAAGACCCCCCGCTTCTGCCCGGACACATGGGCTTCTCGGG	' -	•••	S S	H	SEQ

FIG. 2

(1 of 3)

ATGGCGCCGTCCTCCTGGAACAGAAGCTGTCCCGCCTGGAAGCAAAGCTGAAGCAGGAGAACCGGGAAGCCGGC GGAGGATCGACCTCAACCTGGATATCAGCCCCCAGCGGCCCAGGCCCATTATTGTGATCACTCTAAGCCCTGCTCC ATGGCGCCGTCCTCCCTGGAGCAGAAGCTGTCCCGCCTGGAAGCCAAGCTGAAGCAGGAGAACCGTGAGGCCCGCA GGAGGATCGACCTCAACTTGGATATCAGCCCACAGGGCCCAGGGCCCATTATTGTGATCACTCTAAGCCCTGCTCC 140 09 120 40 100

TCCCCGCAGCACCCCCCCCCCCCCCGCCCCGCCCCGCCACATGCTGGGGGCTCCCGTCAACCCTGTTCACACCCCGCA TCCCCACAGCACCCTACACCCCCCCCCGGCCCCGGCCACATGCTGGGGGCTCCCATCAACCTTGTTCACACGGGCA 300 280

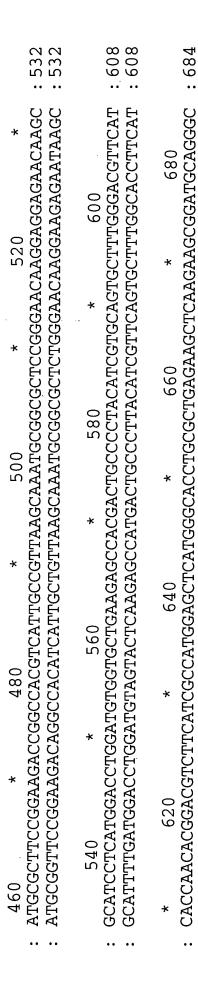
260

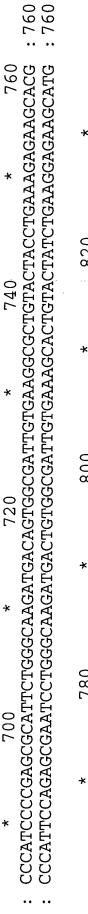
240

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GCGTTATCAGGCAGAAATCAATGACTTGGAGAACTTGGGTGAGATGGGCAGTGGTACCTGTGGTCAGGTGTAGAAG

(2 of 3)





CACCAACACAGACGTCTTTATTGCCATGGAGCTCATGGGCACATGTGCAGAGAAGCTGAAGAAACGAATGCAGGGC



CATCAGCGGCCGCCTGGTGGACTCCAAAGCCAAGACGCGGAGCGCCGGCTGTGCCGCCTACATGGCACCCGAGCGC

FIG. 2

(3 of 3)

AGCTGGCAACAGGACAGTTTCCCTACAAGAACTGCAAGACGGACTTTGAGGTCCTCACCAAAGTCCTACAGGAAGA : 1064 AGCTGGCAACAGGACAGTTCCCCTATAAGAACTGCkAGACGGACTTTGAGGTCCTCACCAAAGTCCTACAGGAAGA : 1064 GCCCCCCCCTTCTGCCCCGGACACATGGGCTTCTCGGGGGACTTCCAGTCCTTCGTCAAAGACTGCCTTACTAAAGAT : 1140 ATCGACCCTCCAGATCCCACCAAGCCTGACTATGACATCCGAGCTGATGTGTGGAGCCTGGGCATCTCACTGGTGG ATTGACCCCCAGACCCCAAGCCGGACTATGACATCCGGGCCGACGTATGGAGCCTGGGCATCTCGTTGGTGG : GCCCCCACTCCTGCCTGGTCACATGGGCTTCTCAGGGGACTTCCAGTCATTTGTCAAAGACTGCCTTACTAAAGAT 1100 1020

CACAGGAAGAGACCAAAGTATAATAAGCTACTTGAACACAGCTTCATCAAGCGCTACGAGACGCTGGAGGTGGACG : 1216 CACAGGAAGAGACCAKAGTATAATAAGCTACTTGAACACAGCTTCATCAAGCACTATGAGATACTCGAGGTGGATG : 1216 1260

1200

1160

TCGCGTCCTGGTTTAAGGATGTCATGGCGAAGACCGAGTCCCCAAGGACTAGTGGAGTCCTGAGTCAGCACCATCT

1300

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